



OIEP

RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/10/042,894A

TIME: 09:54:24

Input Set : A:\1286 AMD SEQLIST.TXT

Output Set: N:\CRF3\06052002\J042894A.raw

ENTERED

4 <110> APPLICANT: Shi, Jinrui
 5 Beach, Larry
 6 Wang, Hongyu
 7 Rafalski, Antoni J.
 8 Cahoon, Rebecca E.
 10 <120> TITLE OF INVENTION: Novel Inositol Polyphosphate Kinase
 11 Genes and Uses Thereof
 13 <130> FILE REFERENCE: 1286
 15 <140> CURRENT APPLICATION NUMBER: US 10/042,894A
 16 <141> CURRENT FILING DATE: 2002-01-09
 18 <150> PRIOR APPLICATION NUMBER: US 60/261,465
 19 <151> PRIOR FILING DATE: 2001-01-12
 21 <160> NUMBER OF SEQ ID NOS: 37
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1169
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Zea mays
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (84)...(806)
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 36 cttgctccca tagtcccat acc atg ccc gac ctc cac ccg ccg gag cac caa 113
 37 Met Pro Asp Leu His Pro Pro Glu His Gln
 38 1 5 10
 40 gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc ccg etc atc gac 161
 41 Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
 42 15 20 25
 44 ggc tcc ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag 209
 45 Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
 46 30 35 40
 48 cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg 257
 49 His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Val Pro
 50 45 50 55
 52 gcc cgc atc oga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc 305
 53 Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
 54 60 65 70
 56 ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc 353
 57 Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
 58 75 80 85 90
 60 gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag 401
 61 Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys

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62          95          100          105
64 atc ggc gcc atc acg tgg cca ccg agt tcg ccg gag ccc tac atc gcc 449
65 Ile Gly Ala Ile Thr Trp Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala
66          110          115          120
68 aag tac ctc gcc aag gac cgc ggg acc acg agc gtt ctg ctc gga ttc 497
69 Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe
70          125          130          135
72 cgc gtc ttg cgt ccg agt cgt ccg ccc cga ggg cgc cgt gtg gcg gac 545
73 Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Val Ala Asp
74          140          145          150
76 gga gcg ccc gga ggt gaa ggc tat gga cac cgt ccg cgt ccg ccg cgt 593
77 Gly Ala Pro Gly Gly Glu Gly Tyr Gly His Arg Arg Pro Pro Arg
78 155          160          165          170
80 gct ccg gcg cta cgt gtc atc cgc ttg ccg acg agg gga tgg act gcg 641
81 Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala
82          175          180          185
84 cgc tcg ccg cgg cgg tgt acg gag gaa aag gtg gag tct tgt cac agc 689
85 Arg Ser Arg Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser
86          190          195          200
88 tgc gcg agc tca agg cat ggt tgg agg agc aga ctc tgt tcc act tct 737
89 Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser
90          205          210          215
92 act ccg cgt cga ttc ttc tgg gct atg atg ctg ctg cag tcg cag cag 785
93 Thr Arg Arg Arg Phe Phe Trp Ala Met Met Leu Leu Gln Ser Gln Gln
94          220          225          230
96 gcg gag gtg ggg gtg ggg taa cagtgaagct ggtggacttt gcccatgtgg 836
97 Ala Glu Val Gly Val Gly *
98 235          240
100 ccgaggggtga tgggggtgatt gaccacaact tctctgggcga gctctgctag ctgatcaagt 896
101 tctgtttctga cattgtttcca gagactcctt agacgcagcc tttgggtcct tcttaagaga 956
102 ggaactctgac atttttgatt tgataacaaa ggaagcactt tcagctgcgaa aaaaagaaaag 1016
103 cagcagtgcg gatgaagatg acagttagtga ggaagattcg gatgatgagc caacaaaagt 1076
104 tgaagaaaag aaggtcccaa aagtatcaga aaacattgga tctgagggatg aatcttctga 1136
105 agacgagagt gataaagaca gtgaagagcc tca
106          1169
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 240
109 <212> TYPE: PRT
110 <213> ORGANISM: Zea mays
111 <400> SEQUENCE: 2
112 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
113 1          5          10          15
114 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
115 20          25          30
116 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
117 35          40          45
118 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
119 50          55          60
120 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
121 65          70          75          80
122

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123 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
124                                     85          90          95
125 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
126                                     100         105         110
127 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp
128                                     115         120         125
129 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser
130                                     130         135         140
131 Arg Arg Pro Arg Gly Arg Arg Val Ala Asp Gly Ala Pro Gly Gly Glu
132 145                                     150         155         160
133 Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val
134                                     165         170         175
135 Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys
136                                     180         185         190
137 Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His
138                                     195         200         205
139 Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe
140                                     210         215         220
141 Trp Ala Met Met Leu Leu Gln Ser Gln Gln Ala Glu Val Gly Val Gly
142 225                                     230         235         240
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 923
147 <212> TYPE: DNA
148 <213> ORGANISM: Zea mays
150 <220> FEATURE:
151 <221> NAME/KEY: CDS
152 <222> LOCATION: (53)...(736)
154 <400> SEQUENCE: 3
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156                                     Met Pro
157                                     1
159 gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc 106
160 Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
161                                     5          10          15
163 agc aag ccg gcc ccg ctc atc gac gcc tcc gcc ctc ttc tac aag ccg 154
164 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
165                                     20         25         30
167 ctc cag gcc gcc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202
168 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
169 35                                     40         45         50
171 ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 250
172 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
173                                     55         60         65
175 ccc cgg ttc cac gcc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298
176 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
177                                     70         75         80
179 gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346
180 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
181                                     85          90          95

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183 gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 394
184 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
185 100 105 110
187 agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg 442
188 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly
189 115 120 125 130
191 acc acg agc gtt ctg ctc gga ttc cgc gtc tcc gcc gtc cga gtc gtc 490
192 Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val
193 135 140 145
195 gtc ccc gag gcc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gct 538
196 Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala
197 150 155 160
199 atg gac acc gtc gcc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc 586
200 Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser
201 165 170 175
203 gct tgc cga cga ggg gat gga ctg cgc gct cgc gcc gcc ggt gta cgg 634
204 Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly Val Arg
205 180 185 190
207 agg aaa agg tgg agt ctt gtc act gct gcg cga gct caa gcc gtg gtt 682
208 Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly Val Val
209 195 200 205 210
211 cga gga gca gcc tct gtt cca ctt cta ctc gcc gtc gat tct tct ggg 730
212 Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser Ser Gly
213 215 220 225
215 cta tga tgctgtgca gtgcgacgag gcggaggtgg ggggtgggta acagtgaagc 786
216 Leu *
219 tgggtgacct tgcccatgtg gccgaggggtg atgggggtgat tgaccacaac ttctgtggcg 846
220 ggctctgtcta gctgatcaag ttctgtttctg acattgttcc agagactcct cagacgcagc 906
221 ctttgggtcc ttcttaa 923
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 227
225 <212> TYPE: PRT
226 <213> ORGANISM: Zea mays
228 <400> SEQUENCE: 4
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230 1 5 10 15
231 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
232 20 25 30
233 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
234 35 40 45
235 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
236 50 55 60
237 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
238 65 70 75 80
239 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
240 85 90 95
241 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
242 100 105 110
243 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp

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115      120      125
245 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
246      130      135      140
247 Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
248 145      150      155      160
249 Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val
250      165      170      175
251 Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly
252      180      185      190
253 Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly
254      195      200      205
255 Val Val Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser
256      210      215      220
257 Ser Gly Leu
258 225
261 <210> SEQ ID NO: 5
262 <211> LENGTH: 923
263 <212> TYPE: DNA
264 <213> ORGANISM: Zea mays
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (53)...(922)
270 <400> SEQUENCE: 5
271 accgcttcca ccatacgccac tcgtcaccac ttgctcccat agtcccata cc atg ccc 58
272      Met Pro
273      1
275 gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc 106
276 Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
277      5      10      15
279 agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 154
280 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
281      20      25      30
283 ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202
284 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
285      35      40      45      50
287 ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 250
288 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
289      55      60      65
291 ccc ccg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298
292 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
293      70      75      80
295 gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346
296 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
297      85      90      95
299 gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc aag tgg cca ccg 394
300 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
301      100      105      110
303 agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg 442
304 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/042,894A

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Input Set : A:\1286 AMD SEQLIST.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 12,283,481,491,598,617,619,626,637
Seq#:18; N Pos. 9,15,47,135,230,335,359,403,415,419,450,480,507,509,518
Seq#:19; N Pos. 85,226,277,294,317,331,351
Seq#:30; Xaa Pos. 3,12,14,15,18,25,27
Seq#:31; Xaa Pos. 3,12,14,15,18,25,27
Seq#:32; Xaa Pos. 3,12,14,15,18,25,27
Seq#:33; Xaa Pos. 3,12,14,15,18,25,27
Seq#:34; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:35; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:36; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:37; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38